

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/521,174  
Source: IFWP  
Date Processed by STIC: 7/5/06

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IFWP

## RAW SEQUENCE LISTING

DATE: 07/05/2006

PATENT APPLICATION: US/10/521,174

TIME: 13:48:42

Input Set : A:\Sequence Listing 8-26-05.txt

Output Set: N:\CRF4\07052006\J521174.raw

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3 <110> APPLICANT: AMANO, Yuichiro
4     SUGIYAMA, Yasuo
5     NISHIDA, Mayumi
6     TAKETOMI, Shigehisa
8 <120> TITLE OF INVENTION: Disease Model Animal Carrying Heterologous PPAR Alpha Gene
Introduced
9     Thereinto And Use Thereof
11 <130> FILE REFERENCE: 2005-0041A/WMC/00279
13 <140> CURRENT APPLICATION NUMBER: 10/521,174
14 <141> CURRENT FILING DATE: 2005-1-14
16 <150> PRIOR APPLICATION NUMBER: JP 2002-206162
17 <151> PRIOR FILING DATE: 2002-07-15
19 <160> NUMBER OF SEQ ID NOS: 9
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1404
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (1)..(1404)
33 <400> SEQUENCE: 1
34 atg gtg gac acg gaa agc cca ctc tgc ccc ctc tcc cca ctc gag gcc      48
35 Met Val Asp Thr Glu Ser Pro Leu Cys Pro Leu Ser Pro Leu Glu Ala
36 1          5          10          15
37 ggc gat cta gag agc ccg tta tct gaa gag ttc ctg caa gaa atg gga      96
38 Gly Asp Leu Glu Ser Pro Leu Ser Glu Phe Leu Gln Glu Met Gly
39          20          25          30
40 aac atc caa gag att tcg caa tcc atc ggc gag gat agt tct gga agc      144
41 Asn Ile Gln Glu Ile Ser Gln Ser Ile Gly Glu Asp Ser Ser Gly Ser
42          35          40          45
43 ttt ggc ttt acg gaa tac cag tat tta gga agc tgt cct ggc tca gat      192
44 Phe Gly Phe Thr Glu Tyr Gln Tyr Leu Gly Ser Cys Pro Gly Ser Asp
45          50          55          60
46 ggc tcg gtc atc acg gac acg ctt tca cca gct tcg agc ccc tcc tcg      240
47 Gly Ser Val Ile Thr Asp Thr Leu Ser Pro Ala Ser Ser Pro Ser Ser
48 65          70          75          80
49 gtg act tat cct gtg gtc ccc ggc agc gtg gac gag tct ccc agt gga      288
50 Val Thr Tyr Pro Val Val Pro Gly Ser Val Asp Glu Ser Pro Ser Gly
51          85          90          95
52 gca ttg aac atc gaa tgt aga atc tgc ggg gac aag gcc tca ggc tat      336
53 Ala Leu Asn Ile Glu Cys Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr
54          100         105         110
55 cat tac gga gtc cac gcg tgt gaa ggc tgc aag ggc ttc ttt cgg cga      384

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56	His	Tyr	Gly	Val	His	Ala	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg	Arg	
57			115					120					125				
58	acg	att	cga	ctc	aag	ctg	gtg	tat	gac	aag	tgc	gac	cgc	agc	tgc	aag	432
59	Thr	Ile	Arg	Leu	Lys	Leu	Val	Tyr	Asp	Lys	Cys	Asp	Arg	Ser	Cys	Lys	
60		130					135					140					
61	atc	cag	aaa	aag	aac	aga	aac	aaa	tgc	cag	tat	tgt	cga	ttt	cac	aag	480
62	Ile	Gln	Lys	Lys	Asn	Arg	Asn	Lys	Cys	Gln	Tyr	Cys	Arg	Phe	His	Lys	
63	145					150					155				160		
64	tgc	ctt	tct	gtc	ggg	atg	tca	cac	aac	gcg	att	cgt	ttt	gga	cga	atg	528
65	Cys	Leu	Ser	Val	Gly	Met	Ser	His	Asn	Ala	Ile	Arg	Phe	Gly	Arg	Met	
66					165					170				175			
67	cca	aga	tct	gag	aaa	gca	aaa	ctg	aaa	gca	gaa	att	ctt	acc	tgt	gaa	576
68	Pro	Arg	Ser	Glu	Lys	Ala	Lys	Leu	Lys	Ala	Glu	Ile	Leu	Thr	Cys	Glu	
69			180						185				190				
70	cat	gac	ata	gaa	gat	tct	gaa	act	gca	gat	ctc	aaa	tct	ctg	gcc	aag	624
71	His	Asp	Ile	Glu	Asp	Ser	Glu	Thr	Ala	Asp	Leu	Lys	Ser	Leu	Ala	Lys	
72		195					200					205					
73	aga	atc	tac	gag	gcc	tac	ttg	aag	aac	ttc	aac	atg	aac	aag	gtc	aaa	672
74	Arg	Ile	Tyr	Glu	Ala	Tyr	Leu	Lys	Asn	Phe	Asn	Met	Asn	Lys	Val	Lys	
75		210				215					220						
76	gcc	cgg	gtc	atc	ctc	tca	gga	aag	gcc	agt	aac	aat	cca	cct	ttt	gtc	720
77	Ala	Arg	Val	Ile	Leu	Ser	Gly	Lys	Ala	Ser	Asn	Asn	Pro	Pro	Phe	Val	
78	225				230				235						240		
79	ata	cat	gat	atg	gag	aca	ctg	tgt	atg	gct	gag	aag	acg	ctg	gtg	gcc	768
80	Ile	His	Asp	Met	Glu	Thr	Leu	Cys	Met	Ala	Glu	Lys	Thr	Leu	Val	Ala	
81				245					250					255			
82	aag	ctg	gtg	gcc	aat	ggc	atc	cag	aac	aag	gag	gcg	gag	gtc	cgc	atc	816
83	Lys	Leu	Val	Ala	Asn	Gly	Ile	Gln	Asn	Lys	Glu	Ala	Glu	Val	Arg	Ile	
84			260					265					270				
85	ttt	cac	tgc	tgc	cag	tgc	acg	tca	gtg	gag	acc	gtc	acg	gag	ctc	acg	864
86	Phe	His	Cys	Cys	Gln	Cys	Thr	Ser	Val	Glu	Thr	Val	Thr	Glu	Leu	Thr	
87		275					280					285					
88	gaa	ttc	gcc	aag	gcc	atc	cca	ggc	ttc	gca	aac	ttg	gac	ctg	aac	gat	912
89	Glu	Phe	Ala	Lys	Ala	Ile	Pro	Gly	Phe	Ala	Asn	Leu	Asp	Leu	Asn	Asp	
90		290				295					300						
91	caa	gtg	aca	ttg	cta	aaa	tac	gga	gtt	tat	gag	gcc	ata	ttc	gcc	atg	960
92	Gln	Val	Thr	Leu	Leu	Lys	Tyr	Gly	Val	Tyr	Glu	Ala	Ile	Phe	Ala	Met	
93	305				310				315						320		
94	ctg	tct	tct	gtg	atg	aac	aaa	gac	ggg	atg	ctg	gta	gcg	tat	gga	aat	1008
95	Leu	Ser	Ser	Val	Met	Asn	Lys	Asp	Gly	Met	Leu	Val	Ala	Tyr	Gly	Asn	
96				325				330					335				
97	ggg	ttt	ata	act	cgt	gaa	ttc	cta	aaa	agc	cta	agg	aaa	ccg	ttc	tgt	1056
98	Gly	Phe	Ile	Thr	Arg	Glu	Phe	Leu	Lys	Ser	Leu	Arg	Lys	Pro	Phe	Cys	
99			340					345				350					
100	gat	atc	atg	gaa	ccc	aag	ttt	gat	ttt	gcc	atg	aag	ttc	aat	gca	ctg	1104
101	Asp	Ile	Met	Glu	Pro	Lys	Phe	Asp	Phe	Ala	Met	Lys	Phe	Asn	Ala	Leu	
102			355				360					365					
103	gaa	ctg	gat	gac	agt	gat	atc	tcc	ctt	ttt	gtg	gct	gct	atc	att	tgc	1152
104	Glu	Leu	Asp	Asp	Ser	Asp	Ile	Ser	Leu	Phe	Val	Ala	Ala	Ile	Ile	Cys	

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105      370      375      380
106 tgt gga gat cgt cct ggc ctt cta aac gta gga cac att gaa aaa atg      1200
107 Cys Gly Asp Arg Pro Gly Leu Leu Asn Val Gly His Ile Glu Lys Met
108 385      390      395      400
109 cag gag ggt att gta cat gtg ctc aga ctc cac ctg cag agc aac cac      1248
110 Gln Glu Gly Ile Val His Val Leu Arg Leu His Leu Gln Ser Asn His
111      405      410      415
112 ccg gac gat atc ttt ctc ttc cca aaa ctt ctt caa aaa atg gca gac      1296
113 Pro Asp Asp Ile Phe Leu Phe Pro Lys Leu Leu Gln Lys Met Ala Asp
114      420      425      430
115 ctc cgg cag ctg gtg acg gag cat gcg cag ctg gtg cag atc atc aag      1344
116 Leu Arg Gln Leu Val Thr Glu His Ala Gln Leu Val Gln Ile Ile Lys
117      435      440      445
118 aag acg gag tcg gat gct gcg ctg cac ccg cta ctg cag gag atc tac      1392
119 Lys Thr Glu Ser Asp Ala Ala Leu His Pro Leu Leu Gln Glu Ile Tyr
120      450      455      460
121 agg gac atg tac      1404
122 Arg Asp Met Tyr
123 465
125 <210> SEQ ID NO: 2
126 <211> LENGTH: 468
127 <212> TYPE: PRT
128 <213> ORGANISM: Homo sapiens
130 <400> SEQUENCE: 2
131 Met Val Asp Thr Glu Ser Pro Leu Cys Pro Leu Ser Pro Leu Glu Ala
132 1      5      10      15
133 Gly Asp Leu Glu Ser Pro Leu Ser Glu Glu Phe Leu Gln Glu Met Gly
134      20      25      30
135 Asn Ile Gln Glu Ile Ser Gln Ser Ile Gly Glu Asp Ser Ser Gly Ser
136      35      40      45
137 Phe Gly Phe Thr Glu Tyr Gln Tyr Leu Gly Ser Cys Pro Gly Ser Asp
138      50      55      60
139 Gly Ser Val Ile Thr Asp Thr Leu Ser Pro Ala Ser Ser Pro Ser Ser
140 65      70      75      80
141 Val Thr Tyr Pro Val Val Pro Gly Ser Val Asp Glu Ser Pro Ser Gly
142      85      90      95
143 Ala Leu Asn Ile Glu Cys Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr
144      100      105      110
145 His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg
146      115      120      125
147 Thr Ile Arg Leu Lys Leu Val Tyr Asp Lys Cys Asp Arg Ser Cys Lys
148      130      135      140
149 Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe His Lys
150 145      150      155      160
151 Cys Leu Ser Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met
152      165      170      175
153 Pro Arg Ser Glu Lys Ala Lys Leu Lys Ala Glu Ile Leu Thr Cys Glu
154      180      185      190
155 His Asp Ile Glu Asp Ser Glu Thr Ala Asp Leu Lys Ser Leu Ala Lys

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```

156          195          200          205
157 Arg Ile Tyr Glu Ala Tyr Leu Lys Asn Phe Asn Met Asn Lys Val Lys
158      210          215          220
159 Ala Arg Val Ile Leu Ser Gly Lys Ala Ser Asn Asn Pro Pro Phe Val
160 225          230          235          240
161 Ile His Asp Met Glu Thr Leu Cys Met Ala Glu Lys Thr Leu Val Ala
162          245          250          255
163 Lys Leu Val Ala Asn Gly Ile Gln Asn Lys Glu Ala Glu Val Arg Ile
164          260          265          270
165 Phe His Cys Cys Gln Cys Thr Ser Val Glu Thr Val Thr Glu Leu Thr
166      275          280          285
167 Glu Phe Ala Lys Ala Ile Pro Gly Phe Ala Asn Leu Asp Leu Asn Asp
168      290          295          300
169 Gln Val Thr Leu Leu Lys Tyr Gly Val Tyr Glu Ala Ile Phe Ala Met
170 305          310          315          320
171 Leu Ser Ser Val Met Asn Lys Asp Gly Met Leu Val Ala Tyr Gly Asn
172          325          330          335
173 Gly Phe Ile Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Cys
174          340          345          350
175 Asp Ile Met Glu Pro Lys Phe Asp Phe Ala Met Lys Phe Asn Ala Leu
176          355          360          365
177 Glu Leu Asp Asp Ser Asp Ile Ser Leu Phe Val Ala Ala Ile Ile Cys
178      370          375          380
179 Cys Gly Asp Arg Pro Gly Leu Leu Asn Val Gly His Ile Glu Lys Met
180 385          390          395          400
181 Gln Glu Gly Ile Val His Val Leu Arg Leu His Leu Gln Ser Asn His
182          405          410          415
183 Pro Asp Asp Ile Phe Leu Phe Pro Lys Leu Leu Gln Lys Met Ala Asp
184          420          425          430
185 Leu Arg Gln Leu Val Thr Glu His Ala Gln Leu Val Gln Ile Ile Lys
186      435          440          445
187 Lys Thr Glu Ser Asp Ala Ala Leu His Pro Leu Leu Gln Glu Ile Tyr
188      450          455          460
189 Arg Asp Met Tyr
190 465

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192 &lt;210&gt; SEQ ID NO: 3

193 &lt;211&gt; LENGTH: 20

194 &lt;212&gt; TYPE: DNA

195 &lt;213&gt; ORGANISM: Artificial Sequence

197 &lt;220&gt; FEATURE:

198 &lt;223&gt; OTHER INFORMATION: Oligonucleotide designed to act as primer for amplifying

human

199 SAP promoter.

201 &lt;400&gt; SEQUENCE: 3

202 actgagtaga agtagcagaa

20

204 &lt;210&gt; SEQ ID NO: 4

205 &lt;211&gt; LENGTH: 20

206 &lt;212&gt; TYPE: DNA

207 &lt;213&gt; ORGANISM: Artificial Sequence

209 &lt;220&gt; FEATURE:



274 cccccggcag tgcctgaa

19

VERIFICATION SUMMARY

DATE: 07/05/2006

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Output Set: N:\CRF4\07052006\J521174.raw

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